## GenCore version 5.1.3 Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

January 6, 2003, 13:55:36; Search time 58 Seconds (without alignments) 6062.518 Million cell updates/sec Run on:

US-09-936-024-2 813

1 gtggcagaaacacccaccta......agcgcttcctcctgtgcac 813 Title: Perfect score: Sequence:

IDENTITY NUC Gapop 10.0 , Gapext 1.0 Scoring table:

381593 seqs, 216252194 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Published\_Applications\_NA: Database :

Ggna\_6/ptodata/2/pubpna/USO0\_PUBCOMB.seq:\*
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(cgn2\_6/ptodata/2/pubpna/USO8\_NEW PUB.seq:\*
(cgn2\_6/ptodata/2/pubpna/USO8\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Description	Sequence 1, Appli	٠.	Sequence 2, Appli	8	Sequence 1. Appli	Sequence 19. Appl	Seguence 32. April	e		Secuence 7. Appli	33	3	8	'n	'n	2	0	-	
Ωχ	US-09-935-727-1	US-09-896-096A-2	US-09-894-924-2	US-09-877-156-18	US-09-840-795-1	US-09-877-156-19	US-09-935-727-32	US-09-896-096A-3	US-09-894-924-3	US-09-877-156-7	US-09-935-727-33	US-09-935-727-3	US-09-935-727-28	US-09-896-096A-5	US-09-894-924-5	US-09-896-096A-10	US-09-894-924-10	US-09-935-727-17	US-09-896-096A-9
0B	10	10	10	10	70	9	2	10	9	20	9	10	9	20	10	9	10	10	10
% Query Match Length DB	1077	1114	1114	1347	1137	1859	903	491	491	459	1550	1667	1796	271	271	283	283	499	226
Ouery Match	100.0	100.0	100.0	100.0	99.66	65.6	63.4	58.2	58.2	56.5	48.2	47.7	47.6	30.2	30.2	29.8	29.8	27.2	26.9
Score	813	813	813	813	809.4	533.4	515.4	473.4	473.4	459	392.2	387,4	387	245.2	245.2	242.2	242.2	220.8	218.8
Result No.	-	8	e	•	'n	w	7	80	σ.	21	11	12	13	14	15	16	17	18	19

Sequence 9. Appli	Sequence 6. Appli	y	8	Sequence 8 Appli	141.	Sequence 18, Appl			9	5.	96	Sequence 101. Ann	92	6	6	è	100			6	8	8	8	86.	Sequence 87, Appl
US-09-894-924-9	US-09-896-096A-6	US-09-894-924-6	8-696-09-8U	US-09-894-924-8	US-09-292-758-141	US-09-935-727-18	US-09-896-096A-7	US-09-894-924-7	US-09-062-113-102	US-09-062-113-97	US-09-062-113-96	US-09-062-113-101	US-09-062-113-92	US-09-062-113-93	US-09-062-113-95	US-09-062-113-10	US-09-062-113-100	US-09-062-113-94	US-10-105-934-3	US-09-062-113-6	US-09-062-113-83	US-09-062-113-84	US-09-062-113-85	US-09-062-113-86	US-09-062-113-87
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26.9	24.6	24.6	23.9	23.9	22.5	22.0	18.7	18.7	12.7	12.7	12.7	12.7	12.7	12.7	12.7	12.7	12.7	12.7	12.7	12.7	12.7	12.7	12.7	12.7	12.7
218.8	200	200	194.2	194.2	183	179	152.2	152.2	103.4	103	103	103	103	103	103	103	103	103	103	103	103	103	103	103	103
20	21	22	23	24	25	56	27	<b>58</b>	29	30	31	32	33	34	35	36	37	38	đ M	40	41	42	43	44	45

## ALIGNMENTS

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US-9935-727-1

Sequence 1, Application US/09935727

Patent No. US2002015058341

GENERAL INFORMATION:

TILLE OF INVENTION: Tumor Necrosis Factor Receptors 6 Alpha and 6 Beta FILE REPERRENCE: PE45472

CURRENT FILING DATE: 2001-08-24

PRIOR APPLICATION NUMBER: 60/33,224

PRIOR APPLICATION NUMBER: 60/252,131

PRIOR APPLICATION NUMBER: 60/252,131

PRIOR APPLICATION NUMBER: 60/225,598

PRIOR APPLICATION NUMBER: 60/225,598

PRIOR APPLICATION NUMBER: 60/16,235

PRIOR APPLICATION NUMBER: 60/16,235

PRIOR APPLICATION NUMBER: 60/16,371

PRIOR PILING DATE: 1999-01-201

PRIOR PILING DATE: 1999-04-27

PRIOR PILING DATE: 1999-01-14

PRIOR PILING DATE: 1999-01-17

PRIOR PILING DATE: 1999-01-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WOMBER OF SEQ ID NOS: 42.
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1
LENGTH: 1077
TYPE: DNA
ORGANISM: Homo sapiens
FRAURE:
NAME/KEY: CDS
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61 GCCAGNGCCCCCCAGGCACCTTNGTGCAGCGGCCGTGCCGCGAGACACCCCCACGACG 120
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  APPLICANT: KIM, KYUNG JIN
APPLICANT: LAWRENCE, DAVID A.
APPLICANT: PITTI. ROBERT
APPLICANT: PITTI. ROBERT
APPLICANT: POT, MARGARET
APPLICANT: TWAS, DANIEL B
APPLICANT: TWAS, DANIEL B
TITLE OF INVENTION: DER3 POLYDEPLIGE, A TNFR HOMOLOG
FILE REFERENCE: P113462 REVISED
CURRENT APPLICATION NUMBER: US/09/896,096A
CURRENT FILING DATE: 2001-06-28
FRIOR APPLICATION NUMBER: US 60/059,288
FRIOR RILING DATE: 1998-09-18
FRIOR APPLICATION NUMBER: US 60/059,288
FRIOR FILING DATE: 1998-07-09-18
FRIOR APPLICATION NUMBER: US 60/059,4640
FRIOR APPLICATION NUMBER: US 60/059,640
FRIOR APPLICATION NUMBER: US 60/059,640
FRIOR FILING DATE: 1998-07-30
SEQ ID NO 2: LENGTH: 1114
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; OTHER INFORMATION: Unknown base
US-09-896-096A-2
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                         NAME/KEY: Unsure
LOCATION: 1090
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                                      Length 1077;
                                  Query Match 100.0%; Score 813; DB 10; Length Best Local Similarity 100.0%; Pred. No. 7.8e-162; Matches 813; Conservative 0; Mismatches 0; Indels
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/US-09-896-096A-2
/Sequence 2, Application US/09896096A
/Sequence No. US20020061559A1
/GENERAL INFORMATION:
/APPLICANT: ASHEMAZI, ANI J
/APPLICANT: BOTSTEIN DAVID
/APPLICANT: GURNEY, AUSTIN L.
; LOCATION: (25)..(924)
US-09-935-727-1
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Pred, No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Description	Sequence	Sequence	Sequence	Sequence	Sequence	Seguence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Seguence
SUMMARIES	US-08-794-796-1	US-09-286-529-18 US-09-286-529-19	US-09-286-529-7	US-08-997-918-47	US-08-974-022-1	US-08-795-445A-1	US-08-795-447A-1	US-08-974-186-1	US-08-795-446B-1	US-08-706-945D-123	US-08-974-022-3	US-08-795-445A-3	US-08-795-447A-3	US-08-974-186-3	US-08-795-446B-3	US-08-706-945D-125	US-08-974-022-5	US-08-795-445A-5	US-08-795-447A-5	US-08-974-186-5	US-08-795-446B-5	US-08-706-945D-127	US-09-042-785A-1	US-09-042-785A-6	US-09-042-785A-24	US-08-959-382-1
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* Query Match Length DB	1164	1859	459	525	2432	2432	2432	2432	2432	2432	1324	1324	1324	1324	1324	1324	1355	1355	1355	1355	1355	1355	3331	759	1815	2186
Query Match	0.007	92.6	56.5	15.9	13.8	13.8	13.8	13.8	13.8	13.8	13.6	13.6	13.6	13.6	13.6	13.6	12.7	12.7	12.7	12.7	12.7	12.7	6.9	9.4	8.4	8.4
Score	813	533.4	459	129.6	112	112	112	112	112	112	110.4	110.4	110.4	110.4	110.4	110.4	103	103	103	103	103	103	92	68	89	68
Result No.		<b>7</b> 1 m	ď	s	9	7	œ	φı	20	11	12	13	14	15	16	5	18	19	20	21	22	53	24	25	56	27

100.0%; Score 813; DB 2; Length 1164; 100.0%; Pred. No. 2.6e-154;

Query Match Best Local Similarity

Sequence 3, Appli sequence 12, Appli sequence 1, Appli Sequence 1, Appli Sequence 11, Appli Sequence 11, Appli Sequence 10, Appli Sequence 10, Appli Sequence 10, Appli Sequence 12, Appli Sequence 12, Appli Sequence 12, Appli Sequence 13, Appli Sequence 13, Appli Sequence 13, Appli Sequence 14, Appli		,
8.4 2612 4 US-09-042-785A-3 8.4 2639 4 US-09-042-785A-22 8.4 3474 4 US-09-042-785A-1 6.7 1164 2 US-09-042-785A-5 6.7 1347 4 US-09-286-29-18 6.4 2793 1 US-08-299-747-1 6.4 2793 1 US-08-529-18 6.3 3796 2 US-08-529-18 6.3 3813 2 US-08-62-298-1 6.3 3813 6 US-08-62-000-3 6.3 3813 6 US-08-65-000-3 6.1 691 5 PCT-US95-05423-1 6.1 8706 2 US-08-26-287-1 6.0 1878 3 US-08-26-26-1	REPARAMENT	XX: linear : TYPE: CDNA :-1
24 24 24 24 24 24 24 24 24 24 24 24 24 2	RESULT 1 Sequence 1, Applic Sequence 1, Applic Sequence 1, Applic Sex 1, Seguence 1, Segue	TOPOLOGY: MOLECULE TY US-08-794-796-1
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Query Match
Best Local Similarity 100.0
Matches 813; Conservative
        ; ORGANISM: Homo sapien
US-09-286-529-18
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 TYPE: DNA
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                                                                                                              241 AACCGIGCCIGCCGCTGCCGCACCGGCTTCTTCGCGCACGCTGGTTTCTGCTTGGAGCAC 300
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TITLE OF INVENTION: NEW MEMBERS OF TWF AND TWFR FAMILIES
FILE REFERRINCE: 1408.003/200130.4395C1
CURRENT APPLICATION NUMBER: U$/09/286,529
CURRENT FILING DATE: 1999-04-05
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 18
LENGTH: 1347
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Patent No. 6297367
GENERAL INFORMATION:
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100.0%; Score 813; DB 4; Length 1347; 100.0%; Pred. No. 2.6e-154; cive 0; Mismatches 0; Indels 0;
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; Patent No. 6297367
; GRNERAL INFORMATION:
; APPLICANT Catherine Tribouley
; TITLE OF INFORMATION:
; FILE REPERENCE: 1408.003/200130.439C1
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endothelial cells; keratinocytes; normal prostate; apoptosis;
prostate tumour tissue; ss.
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particularly of the immune system, substantially altered (whether increased or decreased) levels of TWFR-6 alpha and/or TWFR-6 beta septession can be detected, therefore the TWFR-6 alpha and TWFR-6 beta polypeptides, nucleic acids and antibodies are claimed to be useful in the diagnosis of such disorders. Mutations of the TWFR-6 alpha and TWFR-6 beta genes can also be detected. TWF TWFR polypeptides are also claimed to be useful for identifying ligands which may be useful in the treatment of apoptosis related disorders.
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                                                                                                                                                         Sequence 1077 BP; 196 A; 360 C; 326 G; 195 T; 0 other;
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                                                                                                                                                                                             100.04;
                                                                                                                                                                                   Query Match
Best Local Similarity 100.09
Matches 813; Conservative
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02-AUG-2000; 2000WO-US21287.

WO200110908-A1.

15-FEB-2001.

Homo sapiens.

99US-0147297,

04-AUG-1999;

(AMGE-) AMGEN INC.

Hen H;

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Human; NTR3; tumour necrosis factor receptor; TNF receptor; anti-HIV; antianeanic; immunosupressive; antidiabetic; antivital; antibacrerial; orthogratic; neuroprotective; antianflammatory; anorectic; vasotropic; antircheumatorid; antiarthritic; cerebroprotective; tubercollostatic; gene therapy; cancer; blood disorder; brain disorder; autoimmune disease; infection; ss.
                                                                                                                              388 GCATCGTGTCCCCCCGGCGTGCCCCGGCCACCCCCCCGGACACGCAG 447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CGCGCGGCCTTGCAGCTGAAGCTGCGCGGCTCACGGAGCTCCTGGGGGCGCAGGAC 720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          88 GTGGCAGARACACCCACCTACCCTGGCGGGAGGAGAGAGAGGGGGAGCGGCTGGTGT 147
                                                                       148 GCCCAGTGCCCCCCAGGCACCTTTGTGCAGCGGCCGTGCCGCGGGAGACAGCCCCAGGAGG 207
                                                                                                            TGTGGCCCGTGTCCACCGCCACTACACGCAGTTCTGGAACTACCTGGAGCGCTGCCGC 180
                                                                                                                                                                   TACTGCAACGTCCTCTGCGGGAGCGTGAGGAGGAGGCACGGGCTTGCCACGCACCCAC 240
                                                                                                                                                                                 GCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCGGGCACCCCCAAGACACACAG 360
                                                                                                                                                                                                                                                                                                                                     TGCCAGCCGTGCCCCCCCAGGCACCTTCTCAGCCAGCAGCTCCAGCTCAGAGCAGTGCCAG 420
                                                                                                                                                                                                                                                                                                                                                     448 TGCCAGCATGCCCCCCAGGCACCTTCTCAGCCAGCTCCAGCTCAGAGCAGTAGCCAG 507
                                                                                                                                                                                                                                                                                                                                                                                          CCCCACCGCAACTGCACGCCCTGGCCCTCCAATGTGCCCAGGCTCTTCCTCCCAT 480
                                                                                                                                                                                                                                                                                                                                                                                                            CCCCACCGCAACTGCACGGCCCTGGGCCTCAAAGTGCCCAGGCTCTTCCTCCCCAT 567
                                                                                                                                                                                                                                                                                                                                                                                                                                                 GACACCCYGTGCACCAGCTGCACTGGCTTCCCCCTCAGCACCAGGGTACCAGGAGCTGAG 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GAGTGTGAGCGTGCCGTCATCGACTTTGTGGCTTTCCAGGACATCTCCATCAAGAGGCTG 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            721 GGGGCGCTGCTGCTGCTGCTGCTGCTGCGCGTGCCCAGGATGCCCGGGCTGGAG 780
                                                    GCCCAGTGCCCCCCAGGCACCTTTGTGCAGCGGCCGTGCCGGCGGAGACAGCCCCAAGAAG
60
1 GTGGCAGAAACACCCACCTACCCCTGGCGGACGCAGAGACAGGGGAGCGGCTGGTGTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAP62705 standard; cDNA; 1055 BP.
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The present sequence encodes the tumour necrosis factor (TNP) receptor polypeptide NTR1. The NTR3 polynucleotides and polypeptides are useful for treating diseases such as acquired-immunodeficiarcy syndrome (AIDS), anaemia, autoimmune diseases, cachexia, cancer, cerebral malaria, dispering sheeping sheeping states and states. The states of the states
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New tumor necrosis factor receptor, NTR3, useful for treating cancers, stroke, anemia, obesity, rheumatoid arthritis and transplantation rejection -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Gaps
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100.0%; Score 813; DB 22; Length 1055;
Best Local Similarity 100.0%; Pred. No. 5.1e-145;
Matches 813; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1055 BP; 160 A; 369 C; 340 G; 186 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 128-129; 135pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-191521/19.
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Uge of mature FilNT for treating e.g. acute respiratory distress syndrome, ulcerative colitis or ischemic injury during organ transplantation
                  Cohen FJ, Posada JA, Wierda D;
     (ELIL ) LILLY & CO ELI.
                               WPI; 2000-475441/41.
                                    P-PSDB; AAY96596.
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Human FLINT (also known as osteoprotegrin 3) is a new tumour necrosis factor receptor (TNPR) superfamily member, which binds Fast and LIGHT and prevents Past-Fast interaction, Mature PLINT (mPLINT) inhibits Fast-Fast mediated apoptoric and pro-inflammatory activity. mFLINT is useful for treating acute respiratory distress syndrome, treating or inhibiting culcerative colitis, inhibiting ischemic injury during organ cransplantation or for torgan preservation during transplantation. mFLINT can also be used to treat acute liver failure, inflammation of the liver, abnormal (hepatoryte) apoptosis, sapsis, disorders associated with inflammation, hepatitis, ischemia, hypercoagulation or reperfusion, damage to a cardiac myocyte resulting from abnormal myocaddal ischaemia, type I diabetes, cancer, damage to an innocemt byecander tissue induced to by a chemotherapeutic or therapeutic irradiation, aplastic anaemias, myelodysplastic syndromes and pencytopenic conditions. Example 7; Fig 1A-B; 125pp; English.

Sequence 900 BP; 128 A; 324 C; 304 G; 144 T; 0 other;

481 GACACCCTGTGCACCAGCTGCACTGGCTTCCCCCTCAGCACCAGGGTACCAGGAGCTGAG 540 61 GCCCAGTGCCCCCAGGCACCTTTGTGCAGCGGCCGTGCCGCCGAGACAGGCCCCACGAGG 120 148 CCCAGTCCCCCAGCCACCTTTGTGCAGCGCCGTGCCCCCGAGACAGCCCCACCACG AACCGTGCCTGCCGCTGCCGCCACCGGCTTCTTCGCGCACGCTGGTTTCTGCTTGGAGCAC 300 328 AACCGTGCCTGCCGCTGCCGCACCGGCTTCTTCGCGCACGCTGGTTTCTGCTTGGAGCAC 387 GCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCGGGCACCCCCAGAACACGCAG 360 388 GCATCGTGTCCACCTGGTGCCCGGGGGATTGCCCCGGGCACCCCCAGCACACACGCAG 447 420 421 CCCCACCGCAACTGCACGGCCCTGGGCCTGGCCTCAATGTGCCCAGGCTCTTCCTCCCAT 480 508 CCCCACGGAACTGCACGGCCTGGGCCTGGCCCTCAATGTGCCCAGGCTCTTCCTCCCCAT 567 88 Grescherraceccaecerrececrissecserecersacracesereceseresereseres 147 o; Gaps GTGGCAGAAACACCCACCTACCCTGGCGGGACGCAGAGACAGGGGAGCGGCTGGTGTGCC 60 TGCCAGCCGTGCCCCCCAGGCACCTTCTCAGCCAGCAGCTCCAGAGCAGAGCAGTGCCAG 100.0%; Score 813; DB 21; Length 900; 100.0%; Pred. No. 5.1e-145; tive 0; Mismatches 0; Indels 0; Best Local Similarity 100.0 Query Match -301 361 셠 გ 윩 윱 윱 셞 ò 셤 ઠે 윰 ŝ 셤 È ઠે ŝ Š Š ò

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Ouery Match
100.0%; Score 813; DB 20; Length 903;
Best Local Similarity 100.0%; Pred. No. 5.1e-145;
Matches 813; Conservative 0; Mismatches 0; Indels 0; Gaps

GAGTGTGAGCGTCCGTCATCGACTTTGTGGCTTTCCAGACATCTCCATCAAGAGGCTG 600

541

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This DNA encodes a HUMAN NTR-1 polypeptide, a novel orphan receptor. The protein is related to osteoprotegerin (OFG) and to tumour necrosis factor receptor (TNFR). Host cells transformed with a vector comprising the HUMAN NTR-1 mucleic acid are used for the recombinant expression of the protein. HUMAN NTR-1 proteins and antibodies immuno specific for the protein are useful for disgnosis and treatment of humans and animals, especially muscle disorders, as the receptor is involved in regulation of bone mass and muscle metabolism. HUMAN NTR-1 receptors are also useful used to treat disorders associated with HUMAN NTR-1 imbalance.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HUMAN NTR-1; orphan receptor; osteoprotegerin; OPG; TNFR; human; tumour necrosis factor receptor; muscle disorder; bone mass; screening; muscle metabolism; binding agent; cognate ligand; se.
                                                       661 GGCGCGCCTTGCAGCTGAAGCTGCGTCGGCGGCTCACGGAGCTCCTGGGGGCGCAGGAC 720
                                                                                                                         GGGGCGCTGCTGGTGCGGCTGCTGCTGCTGCGCGTGGCCAGGATGCCCGGGCTGGAG 780
                                                                                                                                                                                          808 9GGGCGCTGCTGGTGCGGGCTGCTGCCTGCCGCGTGGCCAGGATGCCCGGGCTGGAG 867
628 GAGIGIGAGCGIGCCGICAICGACITIGIGGCTITICCAGGACAICTCCAICAAGAGGCIG 687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel orphan human receptor polypeptide and nucleic acid - useful as diagnostic reagents and for treatment of muscle disorders
                                  Orphan receptor (HUMAN NTR-1) polypeptide encoding DNA.
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                                                                                                                                                                                                                                                               868 CGGAGCGTCCGTGGAGCGCTTCCTCCTGTGCAC 900
                                                                                                                                                                                                                                        781 CGGAGGTCCGTGAGCGCTTCCTCCTCTGCAC 813
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                                                                                                                                                                                                                                                                                                                                                              AAX22300 standard; DNA; 903 BP.
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